

RAW SEQUENCE LISTING  
PATENT APPLICATION - US/08/753,750DATE: 09/04/97  
TIME: 14:55:06

INPUT SET: S20107.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Lo, Reggie Y.C.  
6 Schryvers, Anthony B.  
7 Potter, Andrew A  
8  
9 (ii) TITLE OF INVENTION: Transferrin Binding Proteins of  
10 Pasteurella Haemolytica and Vaccines Containing Same  
11  
12 (iii) NUMBER OF SEQUENCES: 52  
13  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: BAKER & BOTTS  
16 (B) STREET: 1299 Pennsylvania Avenue  
17 (C) CITY: Washington  
18 (D) STATE: D.C.  
19 (E) COUNTRY: U.S.A.  
20 (F) ZIP: 20004-2400  
21  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
27  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: US 08/753,750  
30 (B) FILING DATE: 29-NOV-1996  
31 (C) CLASSIFICATION:  
32  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: US 60/008,569  
35 (B) FILING DATE: 01-DEC-1995  
36  
37 (vii) PRIOR APPLICATION DATA:  
38 (A) APPLICATION NUMBER: CA 2,164,274  
39 (B) FILING DATE: 01-DEC-1995  
40  
41 (viii) ATTORNEY/AGENT INFORMATION:  
42 (A) NAME: Remenick, James  
43 (B) REGISTRATION NUMBER: 36,902  
44 (C) REFERENCE/DOCKET NUMBER: 63637-0102  
45  
46 (ix) TELECOMMUNICATION INFORMATION:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/753,750DATE: 09/04/97  
TIME: 14:55:08

INPUT SET: S20107.raw

47 (A) TELEPHONE: (202) 639-7996  
48 (B) TELEFAX: (202) 639-7890  
49  
50  
51 (2) INFORMATION FOR SEQ ID NO:1:  
52  
53 (i) SEQUENCE CHARACTERISTICS:  
54 (A) LENGTH: 2784 base pairs  
55 (B) TYPE: nucleic acid  
56 (C) STRANDEDNESS: single  
57 (D) TOPOLOGY: linear  
58  
59 (ii) MOLECULE TYPE: DNA (genomic)  
60  
61 (vi) ORIGINAL SOURCE:  
62 (A) ORGANISM: Pasteurella haemolytica (tbpA gene)  
63 (B) STRAIN: H196  
64  
65  
66  
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
68  
69 ATGATAATGA AATATCATCA TTTTCGCTAT TCACCTGTTG CCTTAACAGT GTTATTTGCT 60  
70  
71 CTTTCTCATT CATACGGTGC TCGGACTGAA AATAAAAAAA TCGAAGAAAA TAACGATCTA 120  
72  
73 GCTGTTCTGG ATGAAGTTAT TGTGACAGAG AGCCATTATG CTCACGAACG TCAAAACGAA 180  
74  
75 GTAAGTGGCT TGGGGAAAAGT AGTGAAAAAT TATCACGAAA TGAGTAAAAA TCAAATTCTT 240  
76  
77 GGTATTCGTG ATTTAACTCG CTATGACCCT GGTATTTTCGG TGGTGGAACA AGGTCGCGGT 300  
78  
79 GCAAGTAGTG GCTATGCCAT TCGAGGTGTA GATAAAAACC GTGTCAGCTT ACTTGTGAT 360  
80  
81 GGGCTACCAC AAGCGCACAG TTATCATACG CTAGGTTTCAG ATGCTAATGG TGGTGCAATT 420  
82  
83 AATGAGATTG AGTATGAAAA CATTCGTTCA ATTGAGTTAA GCAAAGGAGC AAGTTCTGCG 480  
84  
85 GAATATGGCT CTGGTGCGCA TGGTGGTGCT ATTGGTTTTT GACTAAAGA TGCGCAGGAT 540  
86  
87 ATTATTAAAG AGGGGCAGCA TTGGGGCTTA GATAGTAAGA CCTCTTATGC CAGCAAAAAAT 600  
88  
89 AGCCATTTTTT TACAGTCTAT CGCAGCGGCT GGTGAGGCGG GTGGTTTTGA AGCACTTGTT 660  
90  
91 ATTGCAACTC ACCGACACGG TAAAGAGACC AAAATTCATT CCGAGGCAAA TAAATTAAAA 720  
92  
93 CATAATATTC GCGGTATAAC CGGCTTTGAA AATCGCTACG ACTTTACCCA AATTCCGCAC 780  
94  
95 AGAATGCTCC TGGAGGATCT GCTTTTAATT GTGGAAGATA CTTGCCCAAC ATTAGATTGT 840  
96  
97 ACTCCTCGTG CAAGGGTTAA GTTGAACCGC GATAATTTCC CAGTGAGAAC ATTTCCGGAA 900  
98  
99 TATACGCCTG AAGAGCGCAA ACAGCTTGAG CAGATTCCTT ATCGCACTGA GCAGCTCTCA 960

**INPUT SET: S20107.raw**

100							
101	GCCCAAGAAT	ATACCGGTAA	AGATCGCATT	GCACCAAACC	CTTTAGATTA	CAAGAGTAAT	1020
102							
103	TCTGTTTTTA	TGAAGTTTGG	CTATCACTTC	AACTCGTCTC	ATTATCTTGG	CGCAATCTTA	1080
104							
105	GAAGATACAA	AAACACGCTA	CGATATCCGT	GATATGCAAA	CGCCAGCTTA	CTATACAAAA	1140
106							
107	GACGATATTA	ACTTATCACT	TAGGAAC'TAT	GTTTATGAAG	GGGATAATAT	TTTAGATGGC	1200
108							
109	TTAGTGTTC	AGCCAAGGAT	CCCTTATGGG	TTGCGCTATA	GCCATGTGAA	GTTTTTTGAT	1260
110							
111	GAACGTCACC	ACAAACGTCG	TTTAGGATTC	ACCTATAAAT	ATAAACCAGA	GAATAATCGC	1320
112							
113	TGGTTGGATA	GCATTAAACT	CAGTGCGGAT	AAACAAGATA	TTGAACTATA	TAGCCGGCTA	1380
114							
115	CATCGCTTGC	ATTGTAGCGA	TTATCCTGTG	GTAGATAAAA	ATTGCCGCCC	GACTTTGGAT	1440
116							
117	AAATCTTGGT	CTATGTATCG	AACTGAGCGT	AATAATTACC	AAGAAAAGCA	TCGTGTCATT	1500
118							
119	CATTTAGAAT	TTGATAAAGC	GCTAAATGCT	GGTCAAGGCG	TATTTAACCA	AACCCACAAA	1560
120							
121	CTGAATTTAG	GGTTGGGCTT	TGATCGATTT	AATTCGCTTA	TGGATCATGG	GGATATGACT	1620
122							
123	GCCCAATATA	CCAAAGGCGG	TTATACCAGC	TACCGCGGTA	GAGGGCGTTT	AGATAATCCA	1680
124							
125	TATATTTATC	GCCGCGATCC	ACGCAGTATT	GAAACGGTAT	CTTTGTGTAA	TAATACACGC	1740
126							
127	GGCGACATCT	TAAACTGTGA	ACCGCGTAAA	ATTAAAGGCG	ATAGCCATTT	TGTTAGCTTC	1800
128							
129	CGCGATCTAG	TGATAAGCGA	GTATGTGGAT	TTGGGATTAG	GGGTGCGTTT	TGATCAACAT	1860
130							
131	CGATTTAAAT	CTGATGATCC	GTGGACACTT	AGCCGAAC'TT	ATCGAAATTG	GTCTTGGAAT	1920
132							
133	GGTGGGATTA	CGCTTAAACC	AACAGAGTTT	GTATCGCTTT	CTTATCGCAT	TTCAAACGGT	1980
134							
135	TTTAGAGTGC	CTGCATTCTA	TGAAC'TTTAT	GGTAAACGTG	ATCATATTGG	GCTTAAAGAT	2040
136							
137	AACGAATATG	TGCAACGCGC	GCAACGTAGC	CACCAGTTAG	AGCCAGAAAA	ATCGACTAAT	2100
138							
139	CATGAGATTG	GAGTTAGCTT	TAAAGGTCAA	TTTGGTTACC	TTGAATTTCC	GTAATAACTA	2160
140							
141	TAAAAATATG	ATTGCGACAG	CATGTAAAAG	AATAATACAA	AAATCACACT	GTTTCTATAA	2220
142							
143	CTACCATAAT	ATTCAAGATG	TAGCACTAAA	CGGGATAAAT	TTAGTCGCTA	AATTTGACTT	2280
144							
145	ACACGGTATT	TTATCTATGC	TGCCAGATGG	TTTTTATTCA	TCAGTTGCTT	ATAACCGTGT	2340
146							
147	AAAAGTAAAA	GAGCGGAAAC	TAACCGACTC	AAGACTCGAT	AGCGTAAACG	ATCCTATTCT	2400
148							
149	AGATGCGATT	CAGCCAGCAC	GCTATGTGCT	TGGATTGCGC	TACGATCACC	CAGAAGAAAA	2460
150							
151	ATGGGGAATT	GGCATTACTA	CCACCTATTC	TAAAGCCAAA	AACGCCGATG	AGGTGGCAGG	2520
152							

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/753,750

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153 CACACGTCAT CACGGATACA TCGCGTTGAT TTAGGTGGCA AACTGACCGG TTCTTGGTAC 2580
154
155 ACCCATGATA TTACCGGTTA CATCAATTAT AAAA ACTACA CCTTACGTGG AGGAATTTAT 2640
156
157 AATGTGACTA ATCGTAAATA TTCCACTTGG GAATCAGTGC GCCAATCCGG TGTGAATGCA 2700
158
159 GTAAACCAAG ACCGGGGTAG CAATTACACT CGATTTGGCG CTCCGGGGAG AAATTTTCAGT 2760
160
161 TTAGCATTTG AAATGAAGTT TTAG 2784
162

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Pasteurella haemolytica (TbpA protein)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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180 Met Ile Met Lys Tyr His His Phe Arg Tyr Ser Pro Val Ala Leu Thr
181 1 5 10 15
182
183 Val Leu Phe Ala Leu Ser His Ser Tyr Gly Ala Ala Thr Glu Asn Lys
184 20 25 30
185
186 Lys Ile Glu Glu Asn Asn Asp Leu Ala Val Leu Asp Glu Val Ile Val
187 35 40 45
188
189 Thr Glu Ser His Tyr Ala His Glu Arg Gln Asn Glu Val Thr Gly Leu
190 50 55 60
191
192 Gly Lys Val Val Lys Asn Tyr His Glu Met Ser Lys Asn Gln Ile Leu
193 65 70 75 80
194
195 Gly Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu
196 85 90 95
197
198 Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ala Ile Arg Gly Val Asp Lys
199 100 105 110
200
201 Asn Arg Val Ser Leu Leu Val Asp Gly Leu Pro Gln Ala His Ser Tyr
202 115 120 125
203
204 His Thr Leu Gly Ser Asp Ala Asn Gly Gly Ala Ile Asn Glu Ile Glu
205 130 135 140

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/753,750

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206																	
207	Tyr	Glu	Asn	Ile	Arg	Ser	Ile	Glu	Leu	Ser	Lys	Gly	Ala	Ser	Ser	Ala	
208	145					150					155					160	
209																	
210	Glu	Tyr	Gly	Ser	Gly	Ala	His	Gly	Gly	Ala	Ile	Gly	Phe	Arg	Thr	Lys	
211					165					170					175		
212																	
213	Asp	Ala	Gln	Asp	Ile	Ile	Lys	Glu	Gly	Gln	His	Trp	Gly	Leu	Asp	Ser	
214				180					185					190			
215																	
216	Lys	Thr	Ser	Tyr	Ala	Ser	Lys	Asn	Ser	His	Phe	Leu	Gln	Ser	Ile	Ala	
217			195					200					205				
218																	
219	Ala	Ala	Gly	Glu	Ala	Gly	Gly	Phe	Glu	Ala	Leu	Val	Ile	Ala	Thr	His	
220		210					215					220					
221																	
222	Arg	His	Gly	Lys	Glu	Thr	Lys	Ile	His	Ser	Glu	Ala	Asn	Lys	Leu	Lys	
223	225					230					235					240	
224																	
225	His	Asn	Ile	Arg	Arg	Ile	Thr	Gly	Phe	Glu	Asn	Arg	Tyr	Asp	Phe	Thr	
226					245					250					255		
227																	
228	Gln	Ile	Pro	His	Arg	Met	Leu	Leu	Glu	Asp	Leu	Leu	Leu	Ile	Val	Glu	
229				260					265					270			
230																	
231	Asp	Thr	Cys	Pro	Thr	Leu	Asp	Cys	Thr	Pro	Arg	Ala	Arg	Val	Lys	Leu	
232			275					280					285				
233																	
234	Asn	Arg	Asp	Asn	Phe	Pro	Val	Arg	Thr	Phe	Pro	Glu	Tyr	Thr	Pro	Glu	
235		290					295					300					
236																	
237	Glu	Arg	Lys	Gln	Leu	Glu	Gln	Ile	Pro	Tyr	Arg	Thr	Glu	Gln	Leu	Ser	
238	305					310					315				320		
239																	
240	Ala	Gln	Glu	Tyr	Thr	Gly	Lys	Asp	Arg	Ile	Ala	Pro	Asn	Pro	Leu	Asp	
241					325					330					335		
242																	
243	Tyr	Lys	Ser	Asn	Ser	Val	Phe	Met	Lys	Phe	Gly	Tyr	His	Phe	Asn	Ser	
244				340					345					350			
245																	
246	Ser	His	Tyr	Leu	Gly	Ala	Ile	Leu	Glu	Asp	Thr	Lys	Thr	Arg	Tyr	Asp	
247			355					360					365				
248																	
249	Ile	Arg	Asp	Met	Gln	Thr	Pro	Ala	Tyr	Tyr	Thr	Lys	Asp	Asp	Ile	Asn	
250		370					375					380					
251																	
252	Leu	Ser	Leu	Arg	Asn	Tyr	Val	Tyr	Glu	Gly	Asp	Asn	Ile	Leu	Asp	Gly	
253	385				390						395				400		
254																	
255	Leu	Val	Phe	Lys	Pro	Arg	Ile	Pro	Tyr	Gly	Leu	Arg	Tyr	Ser	His	Val	
256					405					410					415		
257																	
258	Lys	Phe	Phe	Asp	Glu	Arg	His	His	Lys	Arg	Arg	Leu	Gly	Phe	Thr	Tyr	

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/753,750**

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TIME: 14:55:18

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Line

Error

Original Text